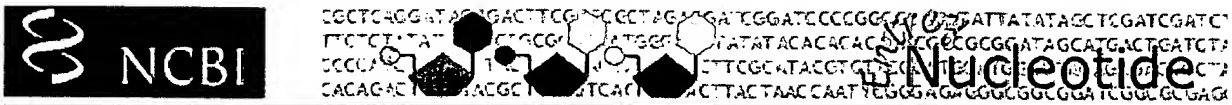

1: AL133463. Human DNA sequenc...[gi:10443352] Links

```
LOCUS       AL133463               84122 bp    DNA     linear   PRI 24-OCT-2002
DEFINITION  Human DNA sequence from clone RP11-149I18 on chromosome 20 Contains
            the 3' end of C20orf82 gene for a novel protein, complete sequence.
ACCESSION   AL133463
VERSION     AL133463.16  GI:10443352
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 84122)
  AUTHORS   Whitehead,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-OCT-2002) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT     On Oct 1, 2000 this sequence version replaced gi:10178396.
            During sequence assembly data is compared from overlapping clones.
            Where differences are found these are annotated as variations
            together with a note of the overlapping clone name. Note that the
            variation annotation may not be found in the sequence submission
            corresponding to the overlapping clone, as we submit sequences with
            only a small overlap as described above.
            The following abbreviations are used to associate primary accession
            numbers given in the feature table with their source databases:
            Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
            on the WORMPEP database can be found at
            http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
            was generated from part of bacterial clone contigs of human
            chromosome 20, constructed by the Sanger Centre Chromosome 20
            Mapping Group.  Further information can be found at
            http://www.sanger.ac.uk/HGP/Chr20
            This sequence was finished as follows unless otherwise noted: all
            regions were either double-stranded or sequenced with an alternate
            chemistry or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by at least
            one plasmid subclone or more than one M13 subclone; and the
            assembly was confirmed by restriction digest. RP11-149I18 is from
            the library RPCI-11.1 constructed by the group of Pieter de Jong.
            For further details see
            http://www.chori.org/bacpac/home.htm
            VECTOR: pBACe3.6
            -------------- Genome Center
            Center: Wellcome Trust Sanger Institute
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: humquery@sanger.ac.uk
            --------------
            IMPORTANT: This sequence is not the entire insert of clone
            RP11-149I18 It may be shorter because we sequence overlapping
```

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            sections only once, except for a short overlap.
            The true left end of clone RP4-585I14 is at 84023 in this sequence.
            The true right end of clone RP5-1077I2 is at 100 in this sequence.
FEATURES              Location/Qualifiers
     source           1..84122
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"
                      /chromosome="20"
                      /clone="RP11-149I18"
                      /clone_lib="RPCI-11.1"
     gene             1..30067
                      /gene="C20orf82"
     mRNA             join(<1..159,9050..9314,17956..18099,21790..21879,
                      28358..30067)
                      /gene="C20orf82"
                      /product="bA149I18.1 (novel protein)"
                      /note="Continues from dJ1077I2.1 in Em:AL050320
                      match: ESTs: Em:AI191256 Em:R44763 Em:W86073 Em:AI082824
                      Em:AI886394 Em:R52250 Em:AV708785 Em:W07772 Em:AV660737
                      Em:BF302850 Em:AW426875 Em:W86257 Em:AW873508 Em:BE287313
                      Em:AW495535 Em:AW435648 Em:AW435639 Em:AL732076"
                      /evidence=not_experimental
     CDS              join(<1..159,9050..9314,17956..18099,21790..21879,
                      28358..28875)
                      /gene="C20orf82"
                      /note="Continues from dJ1077I2.1 in Em:AL050320
                      match: proteins: Tr:Q9H599 Tr:O95432"
                      /codon_start=1
                      /evidence=not_experimental
                      /product="bA149I18.1 (novel protein)"
                      /protein_id="CAC16127.2"
                      /db_xref="GI:13374941"
                      /db_xref="GOA:Q9H599"
                      /db_xref="SPTREMBL:Q9H599"
                      /translation="HQAAHQPFPRPRFRQETGHPSLQRDFPRSFLLDLPNFPDLSKAD
                      INGQNPNIQVTIEVVDGPDSEADKDQHPENKPSWSVPSPDWRAWWQRSLSLARANSGD
                      QDYKYDSTSDDSNFLNPPRGWDHTAPGHRTFETKDQPEYDSTDGEGDWSLWSVCSVTC
                      GNGNQKRTRSCGYACTATESRTCDRPNCPGIEDTFRTAATEVSLLAGSEEFNATKLFE
                      VDTDSCERWMSCKSEFLKKYMHKVMNDLPSCPCSYPTEVAYSTADIFDRIKRKDFRWK
                      DASGPKEKLEIYKPTARYCIRSMLSLESTTLAAQHCCYGDNMQLITRGKGAGTPNLIS
                      TEFSAELHYKVDVLPWIICKGDWSRYNEARPPNNGQKCTESPSDEDYIKQFQEAREY"
     repeat_region    complement(316..456)
                      /note="MER104 repeat: matches 32..176 of consensus"
     repeat_region    453..472
                      /note="4.0 copies 5 mer AAAAC 31% conserved"
     repeat_region    487..505
                      /note="3.8 copies 5 mer AAAAC 38% conserved"
     repeat_region    708..717
                      /note="2.5 copies 4 mer AGGA 20% conserved"
     repeat_region    complement(885..1058)
                      /note="MIR repeat: matches 24..189 of consensus"
     repeat_region    complement(1202..1494)
                      /note="AluJb repeat: matches 1..289 of consensus"
     repeat_region    2597..2608
                      /note="2.0 copies 6 mer ATTCCC 24% conserved"
     repeat_region    2632..2670
                      /note="7.8 copies 5 mer TTTTA 78% conserved"
     repeat_region    complement(2642..2951)
                      /note="AluJo repeat: matches 1..311 of consensus"
     repeat_region    3417..3426
                      /note="2.5 copies 4 mer AAAG 20% conserved"
     repeat_region    3476..3501
                      /note="13.0 copies 2 mer TG 43% conserved"
     repeat_region    3498..3511
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                     /note="2.3 copies 6 mer TGTGCA 28% conserved"
     repeat_region   3512..3538
                     /note="13.5 copies 2 mer CA 29% conserved"
     repeat_region   3950..3967
                     /note="2.2 copies 8 mer CCTCCCCA 27% conserved"
     repeat_region   4082..4106
                     /note="5.0 copies 5 mer CCCCG 25% conserved"
     repeat_region   4908..5154
                     /note="MIR repeat: matches 34..238 of consensus"
     repeat_region   5194..5205
                     /note="2.0 copies 6 mer AGATGA 24% conserved"
     repeat_region   5203..5333
                     /note="MIR3 repeat: matches 2..145 of consensus"
     repeat_region   6382..6398
                     /note="3.4 copies 5 mer TGTTT 25% conserved"
     repeat_region   6560..6569
                     /note="10.0 copies 1 mer A 20% conserved"
     repeat_region   7020..7033
                     /note="2.0 copies 7 mer GATGTAT 28% conserved"
     repeat_region   7036..7048
                     /note="2.6 copies 5 mer CTTTT 26% conserved"
     repeat_region   7060..7073
                     /note="14.0 copies 1 mer T 28% conserved"
     repeat_region   7507..7606
                     /note="MER121 repeat: matches 167..268 of consensus"
     repeat_region   7867..7878
                     /note="2.0 copies 6 mer CACCTG 24% conserved"
     repeat_region   7941..8067
                     /note="MIR repeat: matches 1..140 of consensus"
     repeat_region   complement(8078..8523)
                     /note="MLT1H1 repeat: matches 27..527 of consensus"
     repeat_region   8373..8385
                     /note="2.2 copies 6 mer AATGAA 26% conserved"
     repeat_region   8538..8624
                     /note="MIR repeat: matches 170..262 of consensus"
     repeat_region   8680..8796
                     /note="MLT1H1 repeat: matches 395..518 of consensus"
     repeat_region   8840..8849
                     /note="2.0 copies 5 mer CCCAA 20% conserved"
     repeat_region   9512..9528
                     /note="3.4 copies 5 mer AAATC 25% conserved"
     repeat_region   9751..9760
                     /note="2.0 copies 5 mer AGTGG 20% conserved"
     repeat_region   9808..9819
                     /note="12.0 copies 1 mer C 24% conserved"
     repeat_region   complement(9887..10266)
                     /note="MLT1J2 repeat: matches 6..416 of consensus"
     repeat_region   complement(10536..10673)
                     /note="L2 repeat: matches 3125..3270 of consensus"
     repeat_region   complement(10826..11052)
                     /note="MIR repeat: matches 2..261 of consensus"
     repeat_region   11277..11343
                     /note="MER5A repeat: matches 35..101 of consensus"
     repeat_region   11344..11517
                     /note="MER5A repeat: matches 1..182 of consensus"
     repeat_region   11367..11381
                     /note="2.5 copies 6 mer CCAGAA 21% conserved"
     repeat_region   11520..11698
                     /note="MER5B repeat: matches 2..178 of consensus"
     repeat_region   11773..11825
                     /note="MER5A repeat: matches 136..187 of consensus"
     repeat_region   11978..11989
                     /note="2.0 copies 6 mer CCTAGA 24% conserved"
     repeat_region   complement(12156..12212)
                     /note="MER5A repeat: matches 132..189 of consensus"
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repeat_region   complement(12248..12291)
                /note="MER5A repeat: matches 9..52 of consensus"
repeat_region   12306..12348
                /note="L2 repeat: matches 3271..3313 of consensus"
repeat_region   12337..12350
                /note="3.5 copies 4 mer GAAT 28% conserved"
repeat_region   complement(12443..12595)
                /note="FRAM repeat: matches 1..40 of consensus"
repeat_region   12453..12464
                /note="3.0 copies 4 mer TTTA 24% conserved"
repeat_region   12686..12700
                /note="2.5 copies 6 mer GAAACA 21% conserved"
repeat_region   12995..13005
                /note="2.2 copies 5 mer AGATG 22% conserved"
repeat_region   13397..13552
                /note="MIR repeat: matches 35..193 of consensus"
repeat_region   14129..14138
                /note="2.5 copies 4 mer ACAT 20% conserved"
repeat_region   14157..14167
                /note="2.2 copies 5 mer TTCAC 22% conserved"
repeat_region   complement(14382..14420)
                /note="MLT1H repeat: matches 516..549 of consensus"
repeat_region   14418..14428
                /note="2.2 copies 5 mer CCAGG 22% conserved"
repeat_region   14421..14739
                /note="AluJo repeat: matches 1..310 of consensus"
repeat_region   14712..14739
                /note="28.0 copies 1 mer A 20% conserved"
repeat_region   complement(14740..15136)
                /note="MLT1H repeat: matches 27..516 of consensus"
repeat_region   14796..14826
                /note="3.1 copies 10 mer GTCTGGACTG 35% conserved"
repeat_region   14807..14826
                /note="4.0 copies 5 mer TCTGG 31% conserved"
repeat_region   14830..14841
                /note="2.0 copies 6 mer GGCTGG 24% conserved"
repeat_region   16323..16332
                /note="3.3 copies 3 mer GCA 20% conserved"
repeat_region   complement(16534..16892)
                /note="THE1B repeat: matches 1..364 of consensus"
repeat_region   16900..17163
                /note="L2 repeat: matches 3054..3310 of consensus"
repeat_region   17154..17163
                /note="2.5 copies 4 mer TGGA 20% conserved"
repeat_region   complement(17207..17419)
                /note="MLT1H1 repeat: matches 327..555 of consensus"
repeat_region   17381..17399
                /note="1.9 copies 10 mer AGAAGGCTTG 38% conserved"
repeat_region   17573..17596
                /note="12.0 copies 2 mer TC 32% conserved"
repeat_region   18197..18215
                /note="3.8 copies 5 mer CTTTT 31% conserved"
repeat_region   complement(18198..18489)
                /note="AluSg repeat: matches 13..301 of consensus"
repeat_region   18198..18218
                /note="21.0 copies 1 mer T 24% conserved"
repeat_region   18871..18882
                /note="2.4 copies 5 mer AAACT 24% conserved"
repeat_region   18940..19047
                /note="MER58C repeat: matches 1..132 of consensus"
repeat_region   19015..19028
                /note="4.7 copies 3 mer GAA 21% conserved"
repeat_region   19016..19034
                /note="3.2 copies 6 mer AAGAGA 22% conserved"
repeat_region   19034..19043
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                     /note="3.3 copies 3 mer AGG 20% conserved"
     repeat_region   19040..19117
                     /note="6.5 copies 12 mer AGGAGGAAGAGA 56% conserved"
     repeat_region   19050..19061
                     /note="2.0 copies 6 mer GAAGGG 24% conserved"
     repeat_region   19065..19115
                     /note="17.0 copies 3 mer GGA 66% conserved"
     repeat_region   19103..19197
                     /note="MER58C repeat: matches 119..215 of consensus"
     repeat_region   19679..19694
                     /note="5.3 copies 3 mer GAG 23% conserved"
     repeat_region   19785..20098
                     /note="AluY repeat: matches 2..306 of consensus"
     repeat_region   20083..20097
                     /note="3.8 copies 4 mer AAAG 30% conserved"
     repeat_region   20121..20131
                     /note="2.2 copies 5 mer AAAAT 22% conserved"
     repeat_region   20132..20142
                     /note="3.7 copies 3 mer GAT 22% conserved"
     repeat_region   complement(20136..20382)
                     /note="MIR repeat: matches 8..261 of consensus"
     repeat_region   20797..20807
                     /note="2.2 copies 5 mer CCTGG 22% conserved"
     repeat_region   20968..20977
                     /note="3.3 copies 3 mer CCT 20% conserved"
     repeat_region   complement(21260..21460)
                     /note="MIR repeat: matches 2..219 of consensus"
     repeat_region   21417..21426
                     /note="2.5 copies 4 mer CAGT 20% conserved"
     repeat_region   21536..21546
                     /note="2.8 copies 4 mer AGTG 22% conserved"
     repeat_region   21933..21945
                     /note="2.2 copies 6 mer CTTTTG 26% conserved"
     repeat_region   21973..21988
                     /note="2.7 copies 6 mer TTTCAT 23% conserved"
     repeat_region   22015..22024
                     /note="2.5 copies 4 mer CTTG 20% conserved"
     repeat_region   22257..22270
                     /note="3.5 copies 4 mer GAGG 28% conserved"
     repeat_region   22331..22644
                     /note="AluY repeat: matches 1..302 of consensus"
     repeat_region   22579..22596
                     /note="2.2 copies 8 mer GCACTCCA 36% conserved"
     repeat_region   22624..22641
                     /note="18.0 copies 1 mer A 36% conserved"
     repeat_region   22744..22759
                     /note="2.3 copies 7 mer AGGTGCA 32% conserved"
     repeat_region   22920..22930
                     /note="11.0 copies 1 mer T 22% conserved"
     repeat_region   22989..23014
                     /note="2.0 copies 13 mer TGGGGTCAGGTAA 52% conserved"
     repeat_region   23110..23419
                     /note="AluSq repeat: matches 3..312 of consensus"
     repeat_region   23316..23327
                     /note="2.0 copies 6 mer GGAGGT 24% conserved"
     repeat_region   23391..23424
                     /note="34.0 copies 1 mer A 32% conserved"
     repeat_region   complement(23515..23680)
                     /note="Charlie8 repeat: matches 29..199 of consensus"
     repeat_region   23900..23910
                     /note="2.8 copies 4 mer CAGG 22% conserved"
     repeat_region   complement(23996..24102)
                     /note="LTR33 repeat: matches 415..521 of consensus"
     repeat_region   24141..24155
                     /note="2.5 copies 6 mer GCCACA 30% conserved"
```

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repeat_region   complement(24208..24360)
                /note="MIR repeat: matches 38..192 of consensus"
repeat_region   24502..24512
                /note="3.7 copies 3 mer CAC 22% conserved"
repeat_region   24510..24526
                /note="2.1 copies 8 mer CCAGCCTC 25% conserved"
repeat_region   24858..24870
                /note="2.2 copies 6 mer GCCCCA 26% conserved"
repeat_region   complement(24986..25364)
                /note="LTR16B repeat: matches 1..449 of consensus"
repeat_region   25471..25483
                /note="2.2 copies 6 mer TTTGCC 26% conserved"
repeat_region   25567..25576
                /note="2.5 copies 4 mer ACCC 20% conserved"
repeat_region   25584..25787
                /note="LTR16C repeat: matches 11..241 of consensus"
repeat_region   complement(25792..26153)
                /note="MER92B repeat: matches 272..631 of consensus"
repeat_region   26154..26431
                /note="AluSg repeat: matches 1..278 of consensus"
repeat_region   complement(26432..26701)
                /note="MER92B repeat: matches 2..272 of consensus"
repeat_region   26702..26928
                /note="LTR16C repeat: matches 249..491 of consensus"
repeat_region   26828..26843
                /note="2.0 copies 8 mer TCCCCTGC 32% conserved"
repeat_region   complement(26967..27292)
                /note="MER102b repeat: matches 5..329 of consensus"
repeat_region   27020..27035
                /note="3.2 copies 5 mer GAGCT 23% conserved"
repeat_region   27483..27539
                /note="14.2 copies 4 mer TTAT 46% conserved"
repeat_region   27494..27516
                /note="3.8 copies 6 mer TATTTT 37% conserved"
repeat_region   complement(27522..27831)
                /note="AluSx repeat: matches 1..300 of consensus"
repeat_region   27890..28097
                /note="L1MC4 repeat: matches 7781..8042 of consensus"
repeat_region   28355..28366
                /note="2.0 copies 6 mer CAGACA 24% conserved"
repeat_region   29140..29149
                /note="3.3 copies 3 mer AGA 20% conserved"
repeat_region   29346..29356
                /note="2.8 copies 4 mer AGAA 22% conserved"
repeat_region   29726..29736
                /note="2.2 copies 5 mer AACAA 22% conserved"
repeat_region   29814..29825
                /note="3.0 copies 4 mer AATA 24% conserved"
polyA_signal    29986..29991
                /gene="C20orf82"
polyA_site      30009
                /gene="C20orf82"
repeat_region   30044..30061
                /note="6.0 copies 3 mer ATA 20% conserved"
polyA_signal    30046..30051
                /gene="C20orf82"
polyA_signal    30057..30062
                /gene="C20orf82"
polyA_site      30067
                /gene="C20orf82"
repeat_region   30370..30381
                /note="2.0 copies 6 mer CAATTA 24% conserved"
repeat_region   30475..30484
                /note="2.0 copies 5 mer CCTAG 20% conserved"
repeat_region   complement(30615..30902)
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                     /note="AluSx repeat: matches 3..292 of consensus"
repeat_region        30615..30624
                     /note="10.0 copies 1 mer T 20% conserved"
repeat_region        30846..30855
                     /note="2.5 copies 4 mer CTGC 20% conserved"
repeat_region        30960..30972
                     /note="2.2 copies 6 mer ATATTT 26% conserved"
repeat_region        31037..31047
                     /note="2.2 copies 5 mer TGAAC 22% conserved"
repeat_region        31049..31205
                     /note="L3 repeat: matches 1315..1471 of consensus"
repeat_region        31691..31701
                     /note="2.2 copies 5 mer GGAGG 22% conserved"
misc_feature         complement(31914..32511)
                     /note="match: GSS: Em:BH609834"
repeat_region        complement(32486..32620)
                     /note="MIR repeat: matches 18..153 of consensus"
repeat_region        32635..32647
                     /note="2.6 copies 5 mer CTCTC 26% conserved"
misc_feature         32941..33564
                     /note="match: GSS: Em:AG087240"
repeat_region        33008..33102
                     /note="MIR repeat: matches 2..102 of consensus"
repeat_region        complement(33113..33228)
                     /note="L2 repeat: matches 3176..3313 of consensus"
repeat_region        complement(33296..33702)
                     /note="MLT1J2 repeat: matches 3..447 of consensus"
repeat_region        34127..34395
                     /note="LTR16C repeat: matches 217..491 of consensus"
repeat_region        34442..34468
                     /note="1.9 copies 14 mer TTAATATTTGATAT 54% conserved"
repeat_region        34445..34468
                     /note="3.4 copies 7 mer ATATTTG 39% conserved"
repeat_region        complement(34614..34786)
                     /note="MER5C repeat: matches 1..204 of consensus"
repeat_region        34616..34635
                     /note="20.0 copies 1 mer A 40% conserved"
repeat_region        34922..34937
                     /note="2.3 copies 7 mer ATTTACA 23% conserved"
repeat_region        35912..35939
                     /note="7.0 copies 4 mer TGTT 40% conserved"
repeat_region        35964..35975
                     /note="2.0 copies 6 mer GGAGAA 24% conserved"
repeat_region        35981..36002
                     /note="22.0 copies 1 mer A 44% conserved"
repeat_region        36059..36068
                     /note="2.5 copies 4 mer TCAC 20% conserved"
repeat_region        36134..36144
                     /note="2.2 copies 5 mer TGACT 22% conserved"
repeat_region        complement(36698..36831)
                     /note="L1ME3A repeat: matches 6043..6165 of consensus"
repeat_region        36832..36965
                     /note="L1ME1 repeat: matches 6011..6164 of consensus"
repeat_region        36963..36972
                     /note="2.5 copies 4 mer AAAT 20% conserved"
repeat_region        complement(36986..37465)
                     /note="L1ME3A repeat: matches 5521..6021 of consensus"
repeat_region        complement(37559..37653)
                     /note="L2 repeat: matches 3144..3244 of consensus"
repeat_region        37630..37641
                     /note="3.0 copies 4 mer AATG 24% conserved"
repeat_region        37709..37725
                     /note="2.1 copies 8 mer ATGGGACC 25% conserved"
repeat_region        37960..38052
                     /note="L1M4 repeat: matches 5719..5810 of consensus"
```

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repeat_region   38141..38497
                /note="MLT1A repeat: matches 12..365 of consensus"
repeat_region   38703..38713
                /note="11.0 copies 1 mer A 22% conserved"
repeat_region   38716..40318
                /note="L1MA7 repeat: matches 3866..5480 of consensus"
repeat_region   40328..40617
                /note="AluSq repeat: matches 1..290 of consensus"
repeat_region   40617..40629
                /note="2.2 copies 6 mer ATAGAT 26% conserved"
repeat_region   40623..40699
                /note="19.2 copies 4 mer ATAG 140% conserved"
repeat_region   40687..41480
                /note="L1MA7 repeat: matches 5480..6287 of consensus"
repeat_region   41051..41069
                /note="1.9 copies 10 mer GAACATGGAT 29% conserved"
repeat_region   41478..41487
                /note="2.5 copies 4 mer AATT 20% conserved"
repeat_region   41503..41512
                /note="5.0 copies 2 mer AT 20% conserved"
repeat_region   41680..41726
                /note="2.2 copies 21 mer ATGTGAGTTCACAGCCGGCAT 76%
                conserved"
repeat_region   41785..41798
                /note="3.5 copies 4 mer ACTC 28% conserved"
repeat_region   42030..42046
                /note="2.1 copies 8 mer CTCTCCTG 34% conserved"
repeat_region   complement(42160..42306)
                /note="MIR3 repeat: matches 6..166 of consensus"
repeat_region   42598..42657
                /note="L1MC1 repeat: matches 19..79 of consensus"
repeat_region   42678..43070
                /note="MER57A repeat: matches 8..403 of consensus"
repeat_region   42947..42967
                /note="1.9 copies 11 mer GCTGGAGTGTT 42% conserved"
repeat_region   43071..45020
                /note="L1MC1 repeat: matches 739..2835 of consensus"
repeat_region   43352..43361
                /note="2.5 copies 4 mer AAGA 20% conserved"
repeat_region   43431..43445
                /note="3.0 copies 5 mer GACTG 21% conserved"
repeat_region   43526..43540
                /note="3.0 copies 5 mer AACAG 21% conserved"
repeat_region   43627..43637
                /note="3.7 copies 3 mer AAT 22% conserved"
repeat_region   43902..43911
                /note="5.0 copies 2 mer GA 20% conserved"
repeat_region   44229..44242
                /note="2.3 copies 6 mer ATATCT 28% conserved"
repeat_region   44236..44246
                /note="2.8 copies 4 mer TATC 22% conserved"
repeat_region   44319..44331
                /note="2.2 copies 6 mer AGAATT 26% conserved"
repeat_region   44794..44805
                /note="2.0 copies 6 mer AGTAGC 24% conserved"
repeat_region   45043..45427
                /note="L1MC1 repeat: matches 2894..3283 of consensus"
repeat_region   45361..45375
                /note="2.5 copies 6 mer AAATGA 30% conserved"
repeat_region   45428..48615
                /note="L1MC1 repeat: matches 3487..6608 of consensus"
repeat_region   45700..45710
                /note="2.2 copies 5 mer AATTG 22% conserved"
repeat_region   45705..45720
                /note="2.3 copies 7 mer AATTAAT 23% conserved"
```

```
repeat_region   45838..45847
                /note="3.3 copies 3 mer ATT 20% conserved"
repeat_region   45966..45976
                /note="2.2 copies 5 mer CAAAT 22% conserved"
repeat_region   46056..46066
                /note="2.8 copies 4 mer AATT 22% conserved"
repeat_region   46159..46170
                /note="12.0 copies 1 mer A 24% conserved"
repeat_region   46663..46686
                /note="24.0 copies 1 mer A 21% conserved"
repeat_region   46666..46684
                /note="3.8 copies 5 mer AAAAC 38% conserved"
repeat_region   47369..47380
                /note="2.0 copies 6 mer ATTAAA 24% conserved"
repeat_region   47553..47579
                /note="6.8 copies 4 mer AAAT 54% conserved"
repeat_region   47690..47699
                /note="3.3 copies 3 mer ACA 20% conserved"
repeat_region   48093..48116
                /note="2.4 copies 10 mer GCTATCCAGT 39% conserved"
repeat_region   48639..48649
                /note="11.0 copies 1 mer A 22% conserved"
repeat_region   48671..48681
                /note="2.2 copies 5 mer CAAGG 22% conserved"
repeat_region   48949..48974
                /note="6.5 copies 4 mer AAAG 25% conserved"
repeat_region   49032..49045
                /note="3.5 copies 4 mer AAAC 21% conserved"
repeat_region   49159..49169
                /note="5.5 copies 2 mer CA 22% conserved"
repeat_region   49196..49205
                /note="2.5 copies 4 mer CAGC 20% conserved"
repeat_region   49336..49347
                /note="2.0 copies 6 mer ACAGGG 24% conserved"
repeat_region   49684..49700
                /note="2.1 copies 8 mer TTCCCAAA 25% conserved"
repeat_region   49881..49892
                /note="2.4 copies 5 mer AAAAG 24% conserved"
repeat_region   complement(50138..50332)
                /note="MLT1J repeat: matches 110..316 of consensus"
repeat_region   50333..50631
                /note="AluSx repeat: matches 1..296 of consensus"
repeat_region   complement(50632..50674)
                /note="MLT1J repeat: matches 70..110 of consensus"
repeat_region   50670..50692
                /note="23.0 copies 1 mer A 46% conserved"
repeat_region   50986..51107
                /note="L2 repeat: matches 3200..3311 of consensus"
repeat_region   51192..51203
                /note="2.4 copies 5 mer TCTTT 24% conserved"
repeat_region   51254..51496
                /note="MIR repeat: matches 23..248 of consensus"
repeat_region   51509..51520
                /note="2.0 copies 6 mer AAGTAC 24% conserved"
misc_feature    complement(51715..51941)
                /note="match: STS: Em:Z94397"
repeat_region   52070..52083
                /note="3.5 copies 4 mer ACAG 28% conserved"
repeat_region   52943..52971
                /note="1.9 copies 15 mer TTCAGTATGAAACTA 42% conserved"
repeat_region   53151..53165
                /note="2.1 copies 7 mer AGTATTT 30% conserved"
repeat_region   53181..53190
                /note="3.3 copies 3 mer CTT 20% conserved"
repeat_region   53481..53498
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                     /note="2.0 copies 9 mer AGTAATTGC 27% conserved"
     repeat_region   53889..53900
                     /note="2.0 copies 6 mer AATTTA 24% conserved"
     repeat_region   53985..54005
                     /note="1.9 copies 11 mer TTAATCATGCC 33% conserved"
     repeat_region   complement(54226..54316)
                     /note="MIR3 repeat: matches 93..183 of consensus"
     repeat_region   54679..54692
                     /note="2.0 copies 7 mer AGGTCTC 28% conserved"
     repeat_region   complement(55373..56126)
                     /note="L1ME1 repeat: matches 5301..6016 of consensus"
     repeat_region   55768..55788
                     /note="3.5 copies 6 mer ATGTAT 33% conserved"
     repeat_region   55800..55811
                     /note="2.0 copies 6 mer GTATAT 24% conserved"
     repeat_region   55826..55837
                     /note="2.0 copies 6 mer GTATAT 24% conserved"
     repeat_region   55862..55876
                     /note="2.5 copies 6 mer CCATCT 21% conserved"
     repeat_region   55897..55906
                     /note="2.5 copies 4 mer CATA 20% conserved"
     repeat_region   55900..55911
                     /note="2.0 copies 6 mer ACATAC 24% conserved"
     repeat_region   56128..58383
                     /note="L1PA11 repeat: matches 3889..6164 of consensus"
     repeat_region   57003..57014
                     /note="2.0 copies 6 mer TGGTAC 24% conserved"
     repeat_region   57038..57049
                     /note="2.4 copies 5 mer GAACA 24% conserved"
     repeat_region   58422..58442
                     /note="4.2 copies 5 mer AAAAT 33% conserved"
     repeat_region   complement(58464..58568)
                     /note="L1ME1 repeat: matches 4385..4484 of consensus"
     repeat_region   58465..58474
                     /note="2.5 copies 4 mer TTTC 20% conserved"
     repeat_region   58569..58953
                     /note="MLT1B repeat: matches 5..390 of consensus"
     repeat_region   complement(58954..59374)
                     /note="L1ME1 repeat: matches 3984..4385 of consensus"
     repeat_region   58973..58988
                     /note="2.7 copies 6 mer TTTCAG 25% conserved"
     repeat_region   59002..59013
                     /note="2.0 copies 6 mer TACAAA 24% conserved"
     repeat_region   59144..59153
                     /note="10.0 copies 1 mer T 20% conserved"
     repeat_region   complement(59375..59670)
                     /note="AluSx repeat: matches 1..296 of consensus"
     repeat_region   59375..59386
                     /note="12.0 copies 1 mer T 24% conserved"
     repeat_region   59554..59565
                     /note="2.0 copies 6 mer ATGGAG 24% conserved"
     repeat_region   complement(59671..60619)
                     /note="L1ME1 repeat: matches 2944..3984 of consensus"
     repeat_region   59751..59761
                     /note="2.8 copies 4 mer ATTG 22% conserved"
     repeat_region   60398..60412
                     /note="3.8 copies 4 mer TTTG 30% conserved"
     repeat_region   60724..60733
                     /note="2.5 copies 4 mer CAGA 20% conserved"
     repeat_region   60854..60864
                     /note="2.2 copies 5 mer AATAG 22% conserved"
     repeat_region   60964..60975
                     /note="2.0 copies 6 mer GGAGAA 24% conserved"
     repeat_region   61069..61096
                     /note="2.3 copies 12 mer TTTTGGGGCTTT 38% conserved"
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repeat_region   61090..61104
                /note="15.0 copies 1 mer T 30% conserved"
repeat_region   61102..61142
                /note="MLT1K repeat: matches 550..588 of consensus"
repeat_region   61219..61270
                /note="L2 repeat: matches 3148..3199 of consensus"
repeat_region   61535..61555
                /note="1.9 copies 11 mer GACAATGTTCT 35% conserved"
repeat_region   61577..61586
                /note="2.5 copies 4 mer TTAC 20% conserved"
repeat_region   complement(61638..62601)
                /note="MER45B repeat: matches 4..1038 of consensus"
repeat_region   61670..61681
                /note="2.0 copies 6 mer AAAATG 24% conserved"
repeat_region   62100..62114
                /note="3.0 copies 5 mer GAAAA 30% conserved"
repeat_region   62196..62214
                /note="4.8 copies 4 mer TTCA 22% conserved"
repeat_region   62650..62660
                /note="2.2 copies 5 mer TTTGT 22% conserved"
repeat_region   63923..63934
                /note="2.0 copies 6 mer CATCTA 24% conserved"
repeat_region   64159..64616
                /note="HAL1 repeat: matches 2..462 of consensus"
repeat_region   64516..64526
                /note="2.2 copies 5 mer CACAG 22% conserved"
repeat_region   64698..64708
                /note="2.2 copies 5 mer TTCCC 22% conserved"
repeat_region   64741..64787
                /note="23.5 copies 2 mer CA 85% conserved"
repeat_region   64797..64808
                /note="2.0 copies 6 mer AGATTT 24% conserved"
repeat_region   64975..64987
                /note="3.2 copies 4 mer ATGA 26% conserved"
repeat_region   65055..65549
                /note="HAL1 repeat: matches 986..1516 of consensus"
repeat_region   65205..65223
                /note="3.2 copies 6 mer GCAAAA 29% conserved"
repeat_region   65305..65318
                /note="7.0 copies 2 mer AG 21% conserved"
repeat_region   65589..65838
                /note="MER45C repeat: matches 1..261 of consensus"
repeat_region   65916..66134
                /note="MER45C repeat: matches 706..953 of consensus"
misc_feature    complement(65987..66472)
                /note="match: GSS: Em:AQ538453"
repeat_region   66165..66174
                /note="10.0 copies 1 mer T 20% conserved"
repeat_region   66558..66719
                /note="L3b repeat: matches 1406..1580 of consensus"
repeat_region   67189..67200
                /note="2.4 copies 5 mer AAGGA 24% conserved"
repeat_region   complement(67370..67969)
                /note="MER41B repeat: matches 1..634 of consensus"
repeat_region   67478..67494
                /note="2.1 copies 8 mer TAAAAGAA 25% conserved"
repeat_region   68298..68309
                /note="2.0 copies 6 mer TCACCA 24% conserved"
repeat_region   68299..68318
                /note="2.2 copies 9 mer CACCATCAC 40% conserved"
repeat_region   68327..68362
                /note="18.0 copies 2 mer AC 27% conserved"
repeat_region   68364..68373
                /note="2.5 copies 4 mer CATG 20% conserved"
repeat_region   68405..68415
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                     /note="2.2 copies 5 mer ACAAA 22% conserved"
repeat_region        68443..68453
                     /note="2.2 copies 5 mer AGGAA 22% conserved"
repeat_region        69224..69233
                     /note="2.5 copies 4 mer TATG 20% conserved"
repeat_region        69387..69396
                     /note="2.5 copies 4 mer CAAG 20% conserved"
repeat_region        69403..69415
                     /note="2.2 copies 6 mer AGAACA 26% conserved"
repeat_region        69603..69613
                     /note="2.8 copies 4 mer CTTC 22% conserved"
repeat_region        69620..69847
                     /note="MLT1L repeat: matches 362..614 of consensus"
repeat_region        69906..69916
                     /note="11.0 copies 1 mer T 22% conserved"
repeat_region        complement(69941..70137)
                     /note="L1MA4 repeat: matches 6105..6300 of consensus"
repeat_region        70144..70156
                     /note="2.2 copies 6 mer CTTTTG 26% conserved"
repeat_region        70242..70256
                     /note="5.0 copies 3 mer ATA 21% conserved"
repeat_region        complement(70306..70409)
                     /note="MIR repeat: matches 20..145 of consensus"
misc_feature         70488..71104
                     /note="match: GSS: Em:AG054326"
repeat_region        70763..70970
                     /note="MIR repeat: matches 7..231 of consensus"
repeat_region        complement(71093..71538)
                     /note="MLT1H repeat: matches 61..522 of consensus"
repeat_region        71160..71170
                     /note="2.8 copies 4 mer GTTG 22% conserved"
repeat_region        71237..71246
                     /note="2.5 copies 4 mer TGGC 20% conserved"
repeat_region        71319..71328
                     /note="3.3 copies 3 mer CTC 20% conserved"
repeat_region        71462..71476
                     /note="3.0 copies 5 mer CCCAG 21% conserved"
repeat_region        71697..71718
                     /note="5.5 copies 4 mer TTGT 28% conserved"
repeat_region        71698..71720
                     /note="3.8 copies 6 mer TGTTTG 30% conserved"
repeat_region        71997..72007
                     /note="2.2 copies 5 mer GCCAG 22% conserved"
repeat_region        72980..73015
                     /note="6.0 copies 6 mer CCCCGC 45% conserved"
repeat_region        73221..73231
                     /note="2.8 copies 4 mer AGAA 22% conserved"
repeat_region        73694..73716
                     /note="11.5 copies 2 mer CA 37% conserved"
repeat_region        73726..73736
                     /note="2.2 copies 5 mer TGGAT 22% conserved"
repeat_region        73737..73748
                     /note="2.0 copies 6 mer CCCAAG 24% conserved"
repeat_region        73832..73842
                     /note="2.8 copies 4 mer GGGA 22% conserved"
repeat_region        74777..74788
                     /note="3.0 copies 4 mer TGGC 24% conserved"
repeat_region        75004..75017
                     /note="3.5 copies 4 mer GGGA 28% conserved"
repeat_region        75333..75357
                     /note="25.0 copies 1 mer A 50% conserved"
repeat_region        75705..75715
                     /note="3.7 copies 3 mer CTC 22% conserved"
repeat_region        76973..77273
                     /note="AluSx repeat: matches 1..298 of consensus"
```

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repeat_region   77258..77273
                /note="16.0 copies 1 mer A 32% conserved"
misc_feature    77384..77797
                /note="match: GSS: Em:AQ237590"
repeat_region   77399..77599
                /note="MER20 repeat: matches 1..218 of consensus"
repeat_region   77714..77727
                /note="2.3 copies 6 mer TACTTT 28% conserved"
repeat_region   78125..78136
                /note="2.4 copies 5 mer TTGTC 24% conserved"
repeat_region   78258..78269
                /note="2.0 copies 6 mer TTATTC 24% conserved"
repeat_region   78968..78989
                /note="2.8 copies 8 mer AAAGAAAA 35% conserved"
repeat_region   79074..79286
                /note="L1ME1 repeat: matches 4184..4392 of consensus"
repeat_region   79287..79572
                /note="AluJb repeat: matches 3..306 of consensus"
repeat_region   79476..79488
                /note="2.2 copies 6 mer GAGGCT 26% conserved"
repeat_region   79549..79572
                /note="24.0 copies 1 mer A 21% conserved"
repeat_region   79551..79575
                /note="4.2 copies 6 mer AAAAAC 43% conserved"
repeat_region   79552..79571
                /note="4.0 copies 5 mer AAAAC 31% conserved"
repeat_region   79573..79926
                /note="L1ME1 repeat: matches 4392..4760 of consensus"
repeat_region   79642..79652
                /note="2.8 copies 4 mer GAAA 22% conserved"
repeat_region   79800..79813
                /note="2.3 copies 6 mer CTGACT 28% conserved"
repeat_region   79933..80076
                /note="L1ME1 repeat: matches 5148..5306 of consensus"
repeat_region   80092..80105
                /note="2.3 copies 6 mer ATTTTT 28% conserved"
repeat_region   80103..80114
                /note="6.0 copies 2 mer TA 24% conserved"
repeat_region   complement(80117..80382)
                /note="AluJo repeat: matches 35..288 of consensus"
repeat_region   80283..80295
                /note="2.6 copies 5 mer TTTAT 26% conserved"
repeat_region   80383..80400
                /note="18.0 copies 1 mer A 27% conserved"
repeat_region   80404..80421
                /note="2.2 copies 8 mer AATTTTTA 36% conserved"
repeat_region   80433..81196
                /note="L1ME1 repeat: matches 5325..6148 of consensus"
repeat_region   80691..80702
                /note="3.0 copies 4 mer TTAA 24% conserved"
repeat_region   81117..81130
                /note="4.7 copies 3 mer GTG 28% conserved"
misc_feature    81225..81678
                /note="match: GSS: Em:AQ667566"
repeat_region   81241..81445
                /note="MER3 repeat: matches 1..208 of consensus"
repeat_region   81369..81386
                /note="3.6 copies 5 mer TTTCA 27% conserved"
repeat_region   81382..81401
                /note="2.0 copies 10 mer AATTTAACTG 31% conserved"
repeat_region   81416..81430
                /note="2.1 copies 7 mer TAGCTAC 30% conserved"
repeat_region   81584..81881
                /note="AluSx repeat: matches 1..300 of consensus"
repeat_region   81791..81802
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                     /note="2.0 copies 6 mer CAGAGG 24% conserved"
     repeat_region   81864..81881
                     /note="18.0 copies 1 mer A 36% conserved"
     repeat_region   82185..82207
                     /note="1.9 copies 12 mer AAGAAAATACAC 37% conserved"
     repeat_region   82374..82682
                     /note="AluJo repeat: matches 4..301 of consensus"
     repeat_region   82664..82682
                     /note="19.0 copies 1 mer A 38% conserved"
     repeat_region   82914..82923
                     /note="2.5 copies 4 mer ATGT 20% conserved"
     repeat_region   83196..83772
                     /note="HAL1 repeat: matches 780..1357 of consensus"
     repeat_region   83702..83716
                     /note="3.8 copies 4 mer AAAT 21% conserved"
     repeat_region   83787..84109
                     /note="HAL1 repeat: matches 1417..1762 of consensus"
ORIGIN
        1 caccaggctg cacaccaacc cttccccaga ccgcgattcc gacaagagac ggggcaccct
       61 tcattgcaaa gagatttccc cagatccttt ctccttgatc taccaaactt tccagatctt
      121 tccaaagctg atatcaatgg gcagaatcca aatatccagg taattcttgg cacctggaag
      181 atgggagata acaaaacagt ccatcttttg ttttctgatg attccagtgg aaactgctgc
      241 cttacctcac ttttcttctt aacccccttaa tgattcctgc ttaagatcat gttatctcca
      301 taagaacagt gctgcatttc attaagtgac acccttgatt gtgagatgca caattatttt
      361 gtgaaccact caaaagaaga aaacactacc aattaaagta tgacacacca aggattacaa
      421 gatacatact aatttaagag acagtgaaat ataaaagcaa aacaaaacaa aatagtctga
      481 aatataaaaa caaaacaaaa caaaattgat gaaatgtggc cgttatagga aaaggccaat
      541 ctgacctgtg aatagattgg gcaaatgttt tcaaatatga gttcaaagca ctcaggaaag
      601 ctgtttctct tagtgcccct ctaaacttgc cttggacacc agaaattcct tcacaaagag
      661 acaagcttcc gttactctaa agtatacatg acttacaaaa caataagagg aaggaagttg
      721 agaacaggag ttcctaggag agagatgact atcttccact aagttgggat ctgatgaagc
      781 agtgggaaat gggaggttag ggaaaggggtg actggggtta aaaataataa ctctcaccta
      841 cactgaaata gctcagtata ctttacaaag caaatgttga tcggatttga ccctcccaac
      901 accctcatga aggagacaaa gcccgtgtca tttttctaat actattggta atgcaccaga
      961 tactcaggaa gttactgttt ggtttaccca aagtcacatg gcagtaaata gtagttatag
     1021 ggctcaaatc caggctctca gactcccaac ccacattcag aggcaaactc ctaattttga
     1081 atgttgtttg tacctttctc tgtttcctcc caaagatggt ccccatgatg gttgagagag
     1141 gctcatcccc cgggcaaccc agcccctatc caactctcgt cctcatatgc ctgcttccat
     1201 atttttttta aagatggcct cactcagtca cccaggttag aatacaatgg cacgatcata
     1261 gcttactgca tgcagcccct acctcccagg ctcaagcgat cctcccacct cagcctcccg
     1321 agtagctgga acttcaagtg tgtgccccca catccagctc atttttaat tttttgtaga
     1381 aacagggttt tgccatatcg ctcaggctgg gctcaaactc ctgggctcaa gcgatccccc
     1441 tgcctcagcc tgccaaagtg ctgggattac aagtatgagc caccacagcc agcccatact
     1501 tgtaagcttt gcttccaatt ctttctattt gtataggtgc acctttttctg tacttttttcc
     1561 tctctggacc aaatgccaat ttgcttacat agcagaaagt tcctgaactt ggactcagac
     1621 caattgatcc ttcattaact gcctctctct ccacagacta acaccctctg catgatacgg
     1681 ttttagatca ggtttcgttg acctgagttg ttttgctctt aacaccagca tcatgggagc
     1741 acgcaaatct cactgagaac acttggaata ccaacccccg ctgtatataa aatgctgcat
     1801 taggttatag gaaattgaaa aatgtaagac ctgttccctc caataaatta gatctgtgtg
     1861 aagatcccag ctaccacata aaacagtgct ggagggatca tgaagacaga ggaggaaaag
     1921 cactgtgtcc caaggggtg gatctcaata ggtggaaaga agtcggacag gctctattga
     1981 tggcacagag tgacaaatat tttggaggtc actctttgac aacccatgca cagaaatcac
     2041 tacaagcccc agttaaaatt tctggtgagt cttgtattgt tttaattgat aaattggaaa
     2101 aacaggcctt tggctccaat ggcccctctc cagggactgg ccacgtggtg tgataaagag
     2161 caatggaacc ctttggaata ggtgcagatt ggcaaggaag gcactgactt cataccgttg
     2221 ctcaaccttg tttcctatca tggctcatcc atgtgtttat agatgttctg gttccagaat
     2281 caggcagttc tcatcccaag ggtgtttagg ccatgcccaa aacaatctga agcctgctgt
     2341 ggctagcgct ttttcccaga ggtgggaatg tcacttgggg cataatgctg aggactgagc
     2401 tataatatca gtgtaattga tttaagaatt actaacgcaa agtcatagga aaatgcctgg
     2461 atgcgggaga acggaaggct gccggggact gttccttcat tggaaagtta ttggctgctt
     2521 tgtgcttgaa cccaatttca gacagaactt cttgggatcc cctttctgtc ttctagataa
     2581 atccatctgt ctgaaaattc ccattcccta cctagacctc acttgggtct tttttatttt
     2641 attttatttt attttatttt attttatttt gacaaggtct ttctttgtca cctatgctac
     2701 ggtacagttg tgcaatcatg gcttgttgag gccttgaact cctgggctca agtgatcctc
     2761 ctacctcagc ctcctgagta gctgggacta caggtgtgag ccaccatgcc tagctaatct
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2821 tttttatttt ttgaagagac caggcctcac tgtgttgccc aggctggtct caaactcctg
2881 gcctcaagta attttcctgc ctcagcctct caaaatgcgg ggattataga catgagtcac
2941 tgcaactgac ctgtctttta aaaatattac ttaaatatta gggaaaagct atagcgtaaa
3001 ggctgaaagg cagttgggac tcccagagct gggaacccca gttacccttt gtacagcaaa
3061 gatcaccgta actcccaaga ataaaggttt accatagctc cagatgtgaa tgttattggc
3121 caaatggatt aaaaattaat gcggctccag cctagctact gtcaaagtca acaaatcaaa
3181 aagagtaagc caacaataca tttttgccta ctgcccagtc aagttattct atttctgctc
3241 tatacaatcc ctatcggtta attttctgtg agcaatacag aggggtggag ggtggccagc
3301 attttattga tctgatgacg ttttggccct gaagaaaata aaattgtggt gcgtttctgg
3361 ccttctgttt gtggaagacc acaaaatgtt agtattggtc actcagaaag atgttcaaag
3421 aaagaataaa acaactgcta cccctgggag cccccgcctt ctgttggcgt gtaattgtgt
3481 gtgtgtgtgt gtgtatgtgt gcatgtgcat gcacacaaac acacccacac accacacagc
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3661 cttcctcaga gcactgttct tttgttgaaa tccactggtt tgacacaggg ccgattcagc
3721 ccagcagaca gccctgctgg tccctgacgg tccctgccgg ccccgtcaaa gcattccctc
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3841 agggctcctg gcctcatctg ccccttcccc tggcaacctg cctttgcccc catctggttc
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3961 ccccaccccc tcaggctctg gaagtgtttc ccacgctcca gggctaagga aacagcctgc
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4141 taaaagcccc aacacctgct tctgcagagc attttaactc ccagaagtca ggcagcctcg
4201 gtcccaagtg aatcagacaa ttctatttta agactggctt caagctgtgg aagtgaggag
4261 gggaagaaaa tgcgcaaaat agaacaaaaa tggtctcaga ctactaaact gagtctccat
4321 atgaaattta aaacaatata agaggttggg ttttatcaaa aacaaaaatc attcaggaaa
4381 gaaagtaaat cccccagaac aagttagact ttggtatcct tggctgggtt ttcagtctgc
4441 agctgatagt cagatatcag agacaaaaat ctctgaaata aatgcactgt taggcttact
4501 acattggttc attactacac tagctattca caaccaaaat attctctttt ctggatcaag
4561 ttgagattag tattcatttc aacccatata tttatttctt ttctcccatt aagacggact
4621 taaaaatagt catgtaaagg cctttttttc cttgcacaga catattaaca tggccacagg
4681 cctcttgagc gccacaagat acaatcagat gagttggcca gggttacagt tgtacgtgct
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